CLAIMS:

1. A method for enhancing the solubility of, and promoting the adoption of native folding conformation, of a protein or polypeptide expressed by recombinant DNA techniques in a host cell, the method comprising:

a) providing a first nucleic acid sequence encoding a protein or polypeptide of interest, the protein or polypeptide being substantially insoluble, or biologically inactive, when expressed in a host cell by recombinant DNA techniques;

b) providing a second nucleic acid sequence encoding a peptide extension having a net negative charge, the peptide T7A of Table 1 being specifically excluded;

c) fusing the second nucleic acid sequence to the first nucleic acid sequence in an expression vector such that a fusion protein encoded by the first and second nucleic acid sequences is expressed in the host cell following transformation of the host cell with the expression vector encoding the fusion protein, the peptide extension encoded by the second nucleic acid sequence being positioned at the carboxyl-terminus of the protein or polypeptide of interest;

d) transforming the host cell with the expression vector encoding the fusion protein; and

e) culturing the transformed host cells under conditions appropriate for the expression of the fusion protein.

2. The method of Claim 1 wherein the host cell is a prokaryotic cell.

3. The method of Claim 1 wherein the host cell is a eukaryotic cell.

4. The method of Claim 1, wherein the net negative charge of the peptide extension ranges from −2 to −20.

5. The method of Claim 1, wherein the net negative charge of the peptide extension is from −15 to −20.

6. The method of Claim 1, wherein the net negative charge of the peptide extension is from −10 to −14.

7. The method of Claim 1, wherein the net negative charge of the peptide extension is from −5 to −9.

8. The method of Claim 1, wherein the net negative charge of the peptide extension is from −2 to −4.

9. The method of Claim 1, wherein the peptide extension adopts a non-ordered conformation following expression.

10. The method of Claim 1 wherein the peptide extension comprises about 61 amino acid residues or less.

11. The method of Claim 1, wherein the peptide extension comprises the 57 residue carboxyl-terminal portion of the T7 gene 10B protein, or solubility or activity

promoting portions thereof.

12. The method of Claim 11 wherein the peptide extension further comprises amino acid substituted variants of the 57 residue carboxyl terminal portion of the T7 gene 10B protein, or active portions thereof, which modifications result in the maintenance of a net negative charge of between −2 and −20.

13. The method of Claim 11, wherein the peptide extension is selected from the group consisting of: Peptide T7C, Peptide T7B, Peptide T7B1, Peptide T7B2, Peptide T7B3, Peptide T7B5, Peptide T7B6, Peptide T7B7, Peptide T7B8, Peptide T7B9, Peptide T7B10, Peptide T7B11, Peptide T7B12, Peptide T7B13, Peptide T7A1, Peptide T7A2, Peptide T7A3, Peptide T7A4, and Peptide T7A5.

14. A method for enhancing the solubility, and promoting the adoption of native folding conformation, of a protein or polypeptide expressed by recombinant DNA techniques in a host cell, the method comprising:

a) providing a first nucleic acid sequence encoding a protein or polypeptide of interest, the protein or polypeptide being substantially insoluble, or biologically inactive, when expressed in a host cell by recombinant DNA techniques;

b) providing a second nucleic acid sequence encoding a peptide extension having a net charge ranging from +2 to −20;

c) fusing the second nucleic acid sequence to the first nucleic acid sequence in an expression vector such that a fusion protein encoded by the first and second nucleic acid sequences is expressed in the host cell following

transformation of the host cell with the expression vector encoding the fusion protein, the peptide extension encoded by the second nucleic acid sequence being positioned at the amino-terminus of the protein or polypeptide of interest;

d) transforming the host cell with the expression vector encoding the fusion protein, under conditions appropriate for expression of the fusion protein; and

e) culturing the transformed host cells under conditions appropriate for the expression of the fusion protein.

15. The method of Claim 14 wherein the host cell is a prokaryotic cell.

16. The method of Claim 14 wherein the host cell is a eukaryotic cell.

17. The method of Claim 14, wherein the net charge of the peptide extension is from -15 to -20.

18. The method of Claim 14, wherein the net charge of the peptide extension is from -10 to -14.

19. The method of Claim 14, wherein the net charge of the peptide extension is from -5 to -9.

20. The method of Claim 14, wherein the net charge of the peptide extension is from -1 to -4.

21. The method of Claim 14, wherein the net charge of the peptide extension is from +2 to -1.

22. The method of Claim 14, wherein the peptide extension adopts a non-ordered conformation following expression.

23. The method of Claim 14, wherein the peptide extension comprises the 57 residue carboxyl-terminal portion of the T7 gene 10B protein, or solubility or activity promoting portions thereof.

24. The method of Claim 23 wherein the peptide extension further comprises amino acid substituted variants of the 57 residue carboxyl terminal portion of the T7 gene 10B protein, or active portions thereof, which modifications result in the maintenance of a net charge of between +2 and −20.

25. The method of Claim 23, wherein the peptide extension is selected from the group consisting of: Peptide N1, Peptide N2, Peptide N3, Peptide N4, Peptide N5, Peptide N6, and Peptide N7.

26. A method for enhancing the *in vitro* renaturation of a protein or polypeptide expressed by recombinant DNA techniques in a host cell, a substantial percentage of the expressed protein or polypeptide being localized in inclusion bodies following expression in the host cell, the method comprising:

a) providing a first nucleic acid sequence encoding a protein or polypeptide of interest;

b) providing a second nucleic acid sequence encoding a peptide extension having a net negative charge, the peptide T7A of Table 1 being specifically excluded;

c) fusing the second nucleic acid sequence to the first nucleic acid sequence

in an expression vector such that a fusion protein encoded by the first and second nucleic acid sequences is expressed in a host cell following transformation of the host cell with the expression vector encoding the fusion protein, the peptide extension encoded by the second nucleic acid sequence being positioned at the carboxyl-terminus of the protein or polypeptide of interest;

d) transforming the host cell with the expression vector encoding the fusion protein, under conditions appropriate for expression of the fusion protein;

e) isolating inclusion bodies from lysates of the host cell;

f) contacting the isolated inclusion bodies with a denaturing solution thereby solubilizing the fusion protein comprising the inclusion body; and,

g) suspending the solubilized fusion protein of step f) in a renaturation buffer.

27. The method of Claim 26 wherein the host cell is a prokaryotic cell.

28. The method of Claim 26 wherein the host cell is a eukaryotic cell.

29. The method of Claim 26 further comprising a heat denaturation step.

30. The method of Claim 26, wherein the net negative charge of the peptide extension ranges from −2 to −20.

31. The method of Claim 26, wherein the net negative charge of the peptide extension is from −15 to −20.

32. The method of Claim 26, wherein the net negative charge of the peptide extension is from −10 to −14.

33. The method of Claim 26, wherein the net negative charge of the peptide extension is from −5 to −9.

34. The method of Claim 26, wherein the net negative charge of the peptide extension is from −1 to −4.

35. The method of Claim 26, wherein the peptide extension adopts a non-ordered conformation following expression.

36. The method of Claim 26 wherein the peptide extension comprises about 61 amino acid residues or less.

37. The method of Claim 26, wherein the peptide extension comprises the 57 residue carboxyl-terminal portion of the T7 gene 10B protein, or solubility or activity promoting portions thereof.

38. The method of Claim 37 wherein the peptide extension further comprises amino acid substituted variants of the 57 residue carboxyl terminal portion of the T7 gene 10B protein, or active portions thereof, which modifications result in the maintenance of a net negative charge of between −2 and −20.

39. The method of Claim 37, wherein the peptide extension is selected from the group consisting of: Peptide T7C, Peptide T7B, Peptide T7B1, Peptide T7B2, Peptide T7B3, Peptide T7B5, Peptide T7B6, Peptide T7B7, Peptide T7B8, Peptide T7B9, Peptide T7B10, Peptide T7B11, Peptide T7B12, Peptide T7B13, Peptide T7A1, Peptide T7A2, Peptide T7A3, Peptide T7A4, and Peptide T7A5.

40. A method for enhancing the *in vitro* renaturation of a protein or polypeptide expressed by recombinant DNA techniques in a host cell, a substantial

percentage of the expressed protein or polypeptide being localized in inclusion bodies following expression in the host cell, the method comprising:

a) providing a first nucleic acid sequence encoding a protein or polypeptide of interest;

b) providing a second nucleic acid sequence encoding a peptide extension having a net charge ranging from +2 to −20;

c) fusing the second nucleic acid sequence to the first nucleic acid sequence in an expression vector such that a fusion protein encoded by the first and second nucleic acid sequences is expressed in a host cell following transformation of the host cell with the expression vector encoding the fusion protein, the peptide extension encoded by the second nucleic acid sequence being positioned at the amino-terminus of the protein or polypeptide of interest;

d) transforming the host cell with the expression vector encoding the fusion protein, under conditions appropriate for expression of the fusion protein;

e) isolating inclusion bodies from lysates of the host cell;

f) contacting the isolated inclusion bodies with a denaturing solution thereby solubilizing the fusion protein comprising the inclusion body; and

g) suspending the solubilized fusion protein of step f) in a renaturation buffer.

41. The method of Claim 40 wherein the host cell is a prokaryotic cell.

42. The method of Claim 40 wherein the host cell is a eukaryotic cell.

43. The method of Claim 40 further comprising a heat denaturation step.

44. The method of Claim 40, wherein the net charge of the peptide extension is from −15 to −20.

45. The method of Claim 40, wherein the net charge of the peptide extension is from −10 to −14.

46. The method of Claim 40, wherein the net charge of the peptide extension is from −5 to −9.

47. The method of Claim 40, wherein the net charge of the peptide extension is from −1 to −4.

48. The method of Claim 40, wherein the net charge of the peptide extension is from +2 to −1.

49. The method of Claim 40, wherein the peptide extension adopts a non-ordered conformation following expression.

50. The method of Claim 40, wherein the peptide extension comprises the 57 residue carboxyl-terminal portion of the T7 gene 10B protein, or solubility or activity promoting portions thereof.

51. The method of Claim 50 wherein the peptide extension further comprises amino acid substituted variants of the 57 residue carboxyl terminal portion of the T7 gene 10B protein, or active portions thereof, which modifications result in the maintenance of a net charge of between +2 and −20.

52. The method of Claim 50, wherein the peptide extension is selected from the group consisting of: Peptide N1, Peptide N2, Peptide N3, Peptide N4, Peptide N5, Peptide N6, and Peptide N7.

53. An expression vector comprising a nucleic acid sequence encoding a peptide extension, the peptide extension having a net negative charge ranging from −2 to −20; the expression vector comprising a multiple cloning site for inserting, in-frame with said peptide extension, a nucleic acid sequence encoding a protein or polypeptide of interest, wherein the expression of the nucleic acid sequences yields a fusion protein in which the peptide extension is fused to the carboxyl-terminus of the protein or polypeptide of interest.

54. The vector of Claim 53 which is optimized for use with a prokaryotic cell.

55. The vector of Claim 53 which is optimized for use with a eukaryotic cell.

56. The expression vector of Claim 53, wherein the net charge of the peptide extension is from −15 to −20.

57. The expression vector of Claim 53, wherein the net charge of the peptide extension is from −10 to −14.

58. The expression vector of Claim 53, wherein the net charge of the peptide extension is from −5 to −9.

59. The expression vector of Claim 53, wherein the net charge of the peptide extension is from −2 to −4.

60. The expression vector of Claim 53, wherein the peptide extension adopts a non-ordered conformation following expression.

61. The expression vector of Claim 53 wherein the peptide extension comprises about 61 amino acid residues or less.

62. The expression vector of Claim 53, wherein the peptide extension comprises the 57 residue carboxyl-terminal portion of the T7 gene 10B protein, or solubility or activity promoting portions thereof.

63. The expression vector of Claim 62 wherein the peptide extension further comprises amino acid substituted variants of the 57 residue carboxyl terminal portion of the T7 gene 10B protein, or active portions thereof, which modifications result in the maintenance of a net negative charge of between −2 and −20.

64. The expression vector of Claim 62, wherein the peptide extension is selected from the group consisting of: Peptide T7C, Peptide T7B, Peptide T7B1, Peptide T7B2, Peptide T7B3, Peptide T7B5, Peptide T7B6, Peptide T7B7, Peptide T7B8, Peptide T7B9, Peptide T7B10, Peptide T7B11, Peptide T7B12, Peptide T7B13, Peptide T7A1, Peptide T7A2, Peptide T7A3, Peptide T7A4, and Peptide T7A5.

65. An expression vector comprising a nucleic acid sequence encoding a peptide extension, the peptide extension having a net charge ranging from +2 to −20; the expression vector comprising a multiple cloning site for inserting, in-frame with said peptide extension, a nucleic acid sequence encoding a protein or polypeptide of interest, wherein the expression of the nucleic acid sequences yields a fusion protein in which the peptide extension is fused to the amino-terminus of the protein or polypeptide of interest.

66. The vector of Claim 65 which is optimized for use with a prokaryotic cell.

67. The vector of Claim 65 which is optimized for use with a eukaryotic cell.

68. The expression vector of Claim 65, wherein the net charge of the peptide extension is from -15 to -20.

69. The expression vector of Claim 65, wherein the net charge of the peptide extension is from -10 to -14.

70. The expression vector of Claim 65, wherein the net charge of the peptide extension is from -5 to -9.

71. The expression vector of Claim 65, wherein the net charge of the peptide extension is from +2 to -4.

72. The expression vector of Claim 65, wherein the peptide extension adopts a non-ordered conformation following expression.

73. The expression vector of Claim 65 wherein the peptide extension comprises about 61 amino acid residues or less.

74. The expression vector of Claim 65, wherein the peptide extension comprises the 57 residue carboxyl-terminal portion of the T7 gene 10B protein, or solubility or activity promoting portions thereof.

75. The expression vector of Claim 74 wherein the peptide extension further comprises amino acid substituted variants of the 57 residue carboxyl terminal portion of the T7 gene 10B protein, or active portions thereof, which modifications result in the maintenance of a net charge of between +2 and -20.

76. The expression vector of Claim 74, wherein the peptide extension is selected from the group consisting of: Peptide N1, Peptide N2, Peptide N3, Peptide N4, Peptide N5, Peptide N6, and Peptide N7.

77. A method for enhancing the solubility and promoting the adoption of native folding conformation of a recombinant protein or polypeptide of interest, which protein or polypeptide would otherwise adopt a non-native conformation and form an insoluble inclusion body when expressed by recombinant DNA techniques in a host cell, the method comprising expressing said protein or polypeptide as a fusion protein wherein the protein or polypeptide is fused to a charged peptide extension, said peptide extension comprising 61 amino acid residues or less and which peptide extension confers a self-chaperoning activity to the fusion protein.

78. The method of Claim 77, wherein the peptide extension is fused to the carboxyl-terminus of the protein or polypeptide of interest.

79. The method of Claim 77, wherein the peptide extension is fused to the amino-terminus of the protein or polypeptide of interest.

80. A method for enhancing the solubility of, and promoting the adoption of native folding conformation, of a protein or polypeptide expressed by recombinant DNA techniques in a prokaryotic cell, the method comprising:

a) providing a first nucleic acid sequence encoding a protein or polypeptide of interest, the protein or polypeptide being substantially insoluble, or biologically inactive, when expressed in a prokaryotic cell by recombinant DNA techniques;

b) providing a second nucleic acid sequence encoding a peptide extension having a net negative charge, the peptide T7A of Table 1 being specifically excluded;

c) fusing the second nucleic acid sequence to the first nucleic acid sequence in a prokaryotic expression vector such that a fusion protein encoded by the first and second nucleic acid sequences is expressed in a prokaryotic cell following transformation of the prokaryotic cell with the prokaryotic expression vector encoding the fusion protein, the peptide extension encoded by the second nucleic acid sequence being positioned at the carboxyl-terminus of the protein or polypeptide of interest;

d) transforming the prokaryotic cell with the prokaryotic expression vector encoding the fusion protein; and

e) culturing the transformed prokaryotic cells under conditions appropriate for the expression of the fusion protein.

81. A method for enhancing the solubility, and promoting the adoption of native folding conformation, of a protein or polypeptide expressed by recombinant DNA techniques in a prokaryotic cell, the method comprising:

a) providing a first nucleic acid sequence encoding a protein or polypeptide of interest, the protein or polypeptide being substantially insoluble, or biologically inactive, when expressed in a prokaryotic cell by recombinant DNA techniques;

b) providing a second nucleic acid sequence encoding a peptide extension having a net charge ranging from +2 to −20;

c) fusing the second nucleic acid sequence to the first nucleic acid sequence in a prokaryotic expression vector such that a fusion protein encoded by

the first and second nucleic acid sequences is expressed in a prokaryotic cell following transformation of the prokaryotic cell with the prokaryotic expression vector encoding the fusion protein, the peptide extension encoded by the second nucleic acid sequence being positioned at the amino-terminus of the protein or polypeptide of interest;

d) transforming the prokaryotic cell with the prokaryotic expression vector encoding the fusion protein, under conditions appropriate for expression of the fusion protein; and

e) culturing the transformed prokaryotic cells under conditions appropriate for the expression of the fusion protein.

82. A method for enhancing the *in vitro* renaturation of a protein or polypeptide expressed by recombinant DNA techniques in a prokaryotic cell, a substantial percentage of the expressed protein or polypeptide being localized in inclusion bodies following expression in the prokaryotic cell, the method comprising:

a) providing a first nucleic acid sequence encoding a protein or polypeptide of interest;

b) providing a second nucleic acid sequence encoding a peptide extension having a net negative charge, the peptide T7A of Table 1 being specifically excluded;

c) fusing the second nucleic acid sequence to the first nucleic acid sequence in a prokaryotic expression vector such that a fusion protein encoded by the first and second nucleic acid sequences is expressed in a prokaryotic cell following transformation of the prokaryotic cell with the prokaryotic

expression vector encoding the fusion protein, the peptide extension encoded by the second nucleic acid sequence being positioned at the carboxyl-terminus of the protein or polypeptide of interest;

d) transforming the prokaryotic cell with the prokaryotic expression vector encoding the fusion protein, under conditions appropriate for expression of the fusion protein;

e) isolating inclusion bodies from lysates of the prokaryotic cell;

f) contacting the isolated inclusion bodies with a denaturing solution thereby solubilizing the fusion protein comprising the inclusion body; and,

g) suspending the solubilized fusion protein of step f) in a renaturation buffer.

83. A method for enhancing the *in vitro* renaturation of a protein or polypeptide expressed by recombinant DNA techniques in a prokaryotic cell, a substantial percentage of the expressed protein or polypeptide being localized in inclusion bodies following expression in the prokaryotic cell, the method comprising:

a) providing a first nucleic acid sequence encoding a protein or polypeptide of interest;

b) providing a second nucleic acid sequence encoding a peptide extension having a net charge ranging from +2 to −20;

c) fusing the second nucleic acid sequence to the first nucleic acid sequence in a prokaryotic expression vector such that a fusion protein encoded by the first and second nucleic acid sequences is expressed in a prokaryotic

cell following transformation of the prokaryotic cell with the prokaryotic expression vector encoding the fusion protein, the peptide extension encoded by the second nucleic acid sequence being positioned at the amino-terminus of the protein or polypeptide of interest;

d) transforming the prokaryotic cell with the prokaryotic expression vector encoding the fusion protein, under conditions appropriate for expression of the fusion protein;

e) isolating inclusion bodies from lysates of the prokaryotic cell;

f) contacting the isolated inclusion bodies with a denaturing solution thereby solubilizing the fusion protein comprising the inclusion body; and

g) suspending the solubilized fusion protein of step f) in a renaturation buffer.

84. An antibody which binds specifically to one or more polypeptides selected from the group consisting of: Peptide T7C, Peptide T7B, Peptide T7B1, Peptide T7B2, Peptide T7B3, Peptide T7B4, Peptide T7B5, Peptide T7B6, Peptide T7B7, Peptide T7B8, Peptide T7B9, Peptide T7B10, Peptide T7B11, Peptide T7B12, Peptide T7B13, Peptide T7A, Peptide T7A1, Peptide T7A2, Peptide T7A3, Peptide T7A4, Peptide T7A5, N1, N2, N3, N4, N5, N6, and N7 described in Table 1.

85. The antibody of Claim 84 which is monoclonal.

86. The antibody of Claim 84 which is polyclonal.